

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (Original) A nucleic acid array comprising a plurality of immobilized elements in an array at addressible locations on a substrate, wherein the plurality of elements comprises nucleic acid sequences from a chromosome syntenic strand, and a first set of the elements are from a first species of organism and a second set of the elements are from a second species and the first species and second species are different, and wherein the nucleic acids in the elements from the first species of organism comprise nucleic acid sequences that are homologous to nucleic acid sequences in nucleic acid elements from a syntenic chromosome of the second species of organism.

2. (Original) The array according to claim 1, wherein the nucleic acid in the first and set set of elements is cloned genomic DNA.

3. (Original) The array according to claim 2, wherein the cloned genomic DNA is carried on a vector selected from the group of vectors consisting of yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), mammalian artificial chromosomes (MACs), and phage P1 artificial chromosomes (PACs).

4. (Currently amended) The array according to ~~any of claims 1-3~~ claim 1, wherein at least one organism is selected from the group consisting of rodents, non-

human primates, marine mammals, lagomorphs, porcines, bovines, carnivores, caprines, equines, amphibia, fish, and insects.

5. (Currently amended) The array according to ~~any of claims 1-3~~ claim 1, wherein at least one organism is a non human transgenic mammal or a mammal having a model disease.

6. (Currently amended) The array according to ~~any of claims 1-3~~ claim 1, wherein at least one organism is a human.

7. (Currently amended) The array according to ~~any of claims 1-3~~ claim 1, wherein at least one organism is selected from the group consisting of a gorilla, a chimpanzee, a monkey, a dog, a hamster, a mouse, a rat, a rabbit, a guinea pig, a sheep, a goat, a swine, a cow, a horse, a frog, a toad, a zebra fish, and a fly.

8. (Currently amended) The array according to ~~any of claims 1-3~~ claim 1, wherein the species of organism are human and mouse.

9. (Currently amended) The array according to ~~any of claims 1-8~~ claim 1, wherein the array further comprises a multi-array surface comprising a plurality of non-contiguous arrays, each array comprising the nucleic acid elements of the first set and the nucleic acid elements of the second set.

10. (Currently amended) The array according to ~~any of claims 1-9~~ claim 1, wherein at least one element of nucleic acid of the first species is at least about 50% homologous to at least one element of nucleic acid of the second species.

11. (Currently amended) The array according to ~~any of claims 1-10~~ claim 1, wherein at least one element of nucleic acid of the first species is at least about 70% homologous to at least one element of nucleic acid of the second species.

12. (Currently amended) The array according to ~~any of claims 1-11~~ claim 1, wherein at least one element of nucleic acid of the first species is at least about 90% homologous to at least one element of nucleic acid of the second species.

13. (Currently amended) The array according to ~~any of claims 1-12~~ claim 1, wherein the contains at least one calibration spot.

14. (Currently amended) The array according to ~~any of claims 1-13~~ claim 1, wherein the elements comprise nucleic acid sequences representing at least one chromosome of at least one species.

15. (Currently amended) The array according to ~~any of claims 1-14~~ claim 1, wherein the elements comprise nucleic acid sequences representating a genome of at least one of the species.

16. (Currently amended) The array according to ~~any of claims 9-15~~ claim 9, wherein each of the plurality of non-contiguous arrays is separated from another of the arrays by a barrier.

17. (Original) A method of measuring genotoxicity of a composition or a physical force in an environment to a cell of a species of organism, the method comprising contacting a test cell or a cell population of a first species with the composition or force; obtaining a sample of nucleic acid from the contacted test cell or population; and analyzing the nucleic acid of the sample for abnormalities by hybridizing the nucleic acid

to an array of syntenic nucleic acid immobilized at addressible locations on a substrate, the syntenic array having elements comprising sequences of syntenic nucleic acid from the genome of the first species, and having elements of sequences of syntenic nucleic acid from the genome of at least a second species of organism.

18. (Original) The method according to claim 17, wherein the second species is a human.

19. (Currently amended) The method according to ~~either of claims 17-18~~ claim 17, wherein contacting is adding the composition to the cell or the population, or exposing the cell or the population to the force, wherein the cell or population is in a cell culture.

Claims 20-44 (Cancelled).

45. (Original) A method of identifying the presence and location of a chromosomal abnormality in cells of a subject during progression of a disease, the method comprising obtaining a nucleic acid sample from the cells affected by the disease; and analyzing the sample for chromosomal abnormalities by hybridizing the sample to elements of a first syntenic nucleic acid array having nucleic acid from the genome of a first species, and further hybridizing the sample to elements of a second syntenic nucleic acid array having nucleic acid from the genome of a second species, the elements of the first and second arrays being immobilized on a substrate.

Claim 46-57 (Cancelled).